

SEQUENCE PROTOCOL

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Boehringer Mannheim GmbH
 (B) ROAD: Sandhofer Str. 112-132
 (C) CITY: Mannheim
 (E) COUNTRY: Germany
 (F) POSTAL CODE: 68305

(ii) TITLE OF INVENTION: T cells specific for kidney carcinoma

(iii) NUMBER OF SEQUENCES: 22

(iv) COMPUTER-READABLE FORM:

- (A) DATA CARRIER: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, version # 1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) POSITION: 1..801

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) POSITION: 1..54

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) POSITION: 55..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG 48
 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
 -18 -15 -10 -5

AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA 96
 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
 1 5 10

CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT 144
 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
 15 20 25 30

TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT 192
 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
 35 40 45

00001500-062197
 161290-000000

ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC ACC CTG TTT Ile Gln Gly Tyr Lys Thr Val Thr Asn Glu Val Ala Ser Leu Phe 50 55 60	240
ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 70 75	288
CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg 80 85 90	336
CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 95 100 105 110	384
CAG AAC CCT GAC CCT GGC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 120 125	432
GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val 130 135 140	480
TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 150 155	528
GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 165 170	576
AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175 180 185 190	624
CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 195 200 205	672
CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 210 215 220	720
CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe 225 230 235	768
AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser 240 245	821
GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG AGGGAACCTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCGGCA ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCTTGACAT TCACGGCAGA GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCTGGAG	881
	941
	1001
	1061
	1121
	1181

AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGATACA TAGTATTCTT
 CTTCTCAAGA CGTGGGGGGA TTTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG
 GCGGTGTGTG ATGTCTGTCT GCCGATGCCT TCATTAATAAT

1241
 1301
 1341

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
 -18 -15 -10 -5
 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
 1 5 10
 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
 15 20 25 30
 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
 35 40 45
 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
 50 55 60
 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
 65 70 75
 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
 80 85 90
 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
 95 100 105 110
 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
 115 120 125
 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
 130 135 140
 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
 145 150 155
 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
 160 165 170
 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
 175 180 185 190
 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
 195 200 205
 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
 210 215 220
 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
 225 230 235

Asn Leu Leu Met Thr L Arg Leu Trp Ser Ser
240 245

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..933

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) POSITION: 1..63

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) POSITION: 64..933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GAT ACC TGG CTC	GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA	48
Met Asp Thr Trp Leu	Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala	
-21 -20	-15 -10	
GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA		96
Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr		
-5 1 5 10		
CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC		144
Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His		
15 20 25		
TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT		192
Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Val Glu Phe		
30 35 40		
CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC		240
Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe		
45 50 55		
GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG		288
Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu		
60 65 70 75		
AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC		336
Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala		
80 85 90		
AGC AGC GAA ACT AAC TCC TAC GAG CAG TAC TTC GGG CCG GGC ACC AGG		384
Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg		
95 100 105		
CTC ACG GTC ACA GAG GAC CTG AAA AAC GTG TTC CCA CCC GAG GTC GCT		432
Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala		
110 115 120		

GTG TTT GAG CCA TCA GCA GAG ATC TCC CAC ACC AAG GCC ACA 480
Val Phe Glu Pro Ser Gln Ala Glu Ile Ser His Thr Gln Lys Ala Thr
125 130 135

CTG GTG TGC CTG GCC ACA GGC TTC TAC CCC GAC CAC GTG GAG CTG AGC 528
Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp Ser His Val Glu Leu Ser
140 145 150 155

TGG TGG GTG AAT GGG AAG GAG GTG CAC AGT GGG GTC AGC ACA GAC CCG 576
Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
160 165 170

CAG CCC CTC AAG GAG CAG CCC GCC CTC AAT GAC TCC AGA TAC TGC CTG 624
Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
175 180 185

AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC 672
Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
190 195 200

CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG 720
His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
205 210 215

TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG 768
Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
220 225 230 235

GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA 816
Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
240 245 250

GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC 864
Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
255 260 265

ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC 912
Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
270 275 280

AAG AGA AAG GAT TCC AGA GGC TAG 936
Lys Arg Lys Asp Ser Arg Gly
285 290

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala
-21 -20 -15 -10

Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr
-5 1 5 10

Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His
15 20 25

Leu Tyr Phe Tyr Trp 30 Arg Gln Ile Leu Gly Gln 35 Val Glu Phe 40
 Leu Val Ser Phe Tyr Asn Asn 50 Glu Ile Ser Glu Lys Ser Glu Ile Phe 55
 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly 70 Ser Asn Phe Thr Leu 75
 Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala 90
 Ser Ser Glu Thr Asn Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg 105
 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala 120
 Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr 135
 Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser 155
 Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro 170
 Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu 185
 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn 200
 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu 215
 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu 235
 Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln 250
 Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala 265
 Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val 280
 Lys Arg Lys Asp Ser Arg Gly 290

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC CTC GTC CTT TCT GGT TCT GCA AGG CAA CTG ACC TTT
Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe
295 300

39

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) POSITION: 1..36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGC CTC GCT ACT GGT TCT GCA AGG CAA CTG ACC TTT
Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe
15 20 25

36

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGT GCC AGC AGT GGA ACA GAT TCC TAC GAG CAG TAC TTC
Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Cys Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGT GCC AGC AGT GAA ACA GAT TCC TAC GAG CAG TAC TTC
Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Cys Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGT GCC AGC AGT GGA ACA GCT TCC TAC GAG CAG TAC TTC
Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Cys Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) POSITION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TGT GCC AGC AGT GGT ACA AAC TCC TAC GAG CAG TAC TTT
Cys Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) TYPE OF MOLECULE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Cys Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..39

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGT GCC ACC TCC GGG ACA GCT TCC TAC GAG CAG TAC TTC
Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
15 20 25

39

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) TYPE OF MOLECULE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Cys Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) POSITION: 1..39

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGT GCC AGA TCC GGG ACA GGC TCC TAC GAG CAG TAC TTC
Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe
15 20 25

39

0001500.002497

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Cys Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strand
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACTGAAGAT CCATCATCTG

20

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strand
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TAGAGGATGG TGGCAGACAG

20

00001509-002497
207250-00510000